

O P E  
OCT 26 2004  
TRADEMARK OFFICE  
Sequence Listing 015181-1 US rev 09-14-04.txt

SEQUENCE LISTING

<110> WOULFE, SUSAN L.  
JAIN, RITA  
BURR, AIMEE

<120> ENGINEERED FAB' FRAGMENT ANTI-TUMOR  
NECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING  
ANTI-RHEUMATIC DRUGS

<130> 122294-1010

<140> US/10/728,420

<141> 2003-12-05

<150> US 60/431,053

<151> 2002-12-05

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<223> Mouse monoclonal antibody hTNF40 CDRH3

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gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn	
20 25 30	

gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc	144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile	
35 40 45	

tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga	192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly	
50 55 60	

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc	288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu	
85 90 95	

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gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg	144
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Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val	
50 55 60	
aag ggc aga ttc acg ttc tct cta gac aca tcc aag tca aca gca tac	240
Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr	
65 70 75 80	
ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc	336
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Leu Val Thr Val Ser Ser	
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Sequence Listing 015181-1 US rev 09-14-04.txt

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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
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<223> Human hTNF40 framework H1

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Sequence Listing 015181-1 US rev 09-14-04.txt

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Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg  
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Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15

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gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat	96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn	
20 25 30	
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Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Asn	
35 40 45	
tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc	192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly	
50 55 60	
agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser	
65 70 75 80	
gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc	288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu	
85 90 95	
acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt	324
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aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat	96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr	
20 25 30	

gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg	144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met	
35 40 45	

ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc	192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe	
50 55 60	

aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt	240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe	
65 70 75 80	

ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt	288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys	
85 90 95	

gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc	336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr	
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Ser Val Thr Val Ser Ser  
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cttggctctg acgtacgagt cagg 84

<210> 102  
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1 5 10 15

aag act gct ata gca att g 67  
Lys Thr Ala Ile Ala Ile  
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Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
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a atg aag aag act gct ata gca att g 69  
Met Lys Lys Thr Ala Ile Ala Ile  
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Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
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20 25 30  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110  
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125  
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140  
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160  
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175  
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
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<223> Synthetic CDP870 Heavy chain mature protein sequence

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
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 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
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 50 55 60  
 Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
 115 120 125  
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
 130 135 140  
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
 145 150 155 160  
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
 165 170 175  
 Ser Ser Gly Leu Tyr Ser Leu Ser Val Val Thr Val Pro Ser Ser  
 180 185 190  
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
 195 200 205  
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220  
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<212> DNA

<213> Artificial sequence

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<223> Synthetic CDP870 nucleic acid sequence (sense strand)

<400> 116

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 accatcaactt gtaaagccag tcagaacgta ggtactaacg tagcctggta tcagcaaaa 180  
 ccaggtaaag ccccaaaagc cctcatctac agtgcctctt tcctctatag tggtgtacca 240  
 tacaggttca gcgatccgg tagtggtaact gatttcaccc tcacgactag tagcctccag 300  
 ccagaagatt tcgccactta ttactgtcaa cagtataaca tctacccact cacattcggt 360  
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 ccatctgtatc agcgttcaa atctgaaact gcctctgtg tggctgtctt gaataacttc 480  
 tatcccagag aggccaaagt acagtggaaag gtggataacg cccttcaatc gggtaactcc 540  
 caggagatgt tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600  
 acgctgagga aagcagacta cgagaaacac aaagcttacg cctgcgaagt caccatcag 660  
 ggcctgagct caccatgtttt aatagaggag agtgggttggagg agggaaaaaaa 720  
 aatgaagaaa actgctatacg caattgcagt ggcgtactat ggttcgcca ccgtggcgca 780  
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catctgcaac gtgaatcaca agcccgaa caccaaggc cacaagaaag ttgagccaa 1440  
atcttgtac aaaactcaca catcgccgc gtatga 1477

<210> 117

<211> 1477

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic CDP870 nucleic acid sequence (anti-sense strand)

<400> 117

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